

REMARKS

Favorable reconsideration is respectfully requested.

The claims are 1 to 23.

The above amendment is responsive to points set forth in the Official Action.

In this regard, a new Title and Abstract have been provided.

Additionally, new claims 17 to 23 are presented in order to more particularly claim what applicants regard as their invention. Claims 17 and 18 are new independent apparatus claims directed at specific features disclosed in the originally filed Specification, see particularly Examples 2, 3, 4 and 6. Claims 19 to 23 are directed to a method of generating an array. Again, the features of all these claims are disclosed in the originally filed Specification, see particularly Example 3; Example 5; and page 11.

In reply to the rejection of claims 1 to 16 under 35 USC 112 as indefinite, the above amendment clarifies the rejected terminology.

If it was not clear before, it is now clear that what is provided attached to the surface of the support is an array of oligonucleotides comprising the whole or a chosen (selected) part of a complete set of oligonucleotides of chosen (selected) lengths. In claims 2 and 9, it is now explained that the set of oligonucleotides of chosen lengths corresponds to the polynucleotide sequences whose differences are being studied.

Claims 1 to 3, 6 and 8 to 10 have been rejected under 35 USC 102(b) as being anticipated by Brigati et al.

Further, claims 1 to 4 and 8 to 11 have been rejected under 35 USC 102(b) as being anticipated by Saiki et al.

These rejections are respectfully traversed.

A brief discussion of the present invention will be of assistance in appreciating applicants' reasons for traversal of

the rejection.

In the subject invention, the unknown, that is to say the polynucleotide which is being analyzed for differences e.g. mutations or whose sequence is being determined, is initially in solution. It is the unknown that is labelled and then applied to the array of immobilized oligonucleotides. The sequences of the immobilized oligonucleotides in the array are at least partially known. Often they are completely known. This is implied by reciting in all claims that different oligonucleotides occupy separate cells of the array; this would not be possible if the sequences of the oligonucleotides were not at least partly known.

In both the references applied by the Examiner, the unknown is immobilized on a support, and probed by labelled hybridization probes of known sequence. This is a fundamental difference.

Turning to Brigati, this reference performs in situ hybridization using biotin-labelled probes. Each slide subjected to the assay procedure, carries one unknown viral DNA gene. There is no teaching or suggestion to form an array of immobilized oligonucleotides. Even if several separate slides carrying different genes could be said to form an array, there is no teaching to provide a different oligonucleotide at each separate cell of the array. Applicants use of the term "cells" in their claims is obviously in a mathematical sense, cells of an array, as opposed to the biological sense "cells of an organism" in which the term is used by Brigati.

With regard to the rejection on Saiki, this reference performs in situ hybridizations. The sample is amplified by PCR, applied to a membrane, and probed with allele-specific oligonucleotides. Several different samples may be applied in separate spots to the membrane, and it is acknowledged that the separate spots constitute an array. However, there is no teaching or suggestion that the array should comprise the whole or

a chosen part of a complete set of oligonucleotides of chosen lengths, the different oligonucleotides occupying separate cells of the array.

For the foregoing reasons, it is considered that the rejections on prior art are untenable and should be withdrawn.

No further issues remaining, allowance of this application is respectfully requested.

If the Examiner has any comments or proposals for expediting prosecution, he is invited to contact the undersigned at the telephone number below.

Respectfully submitted,

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